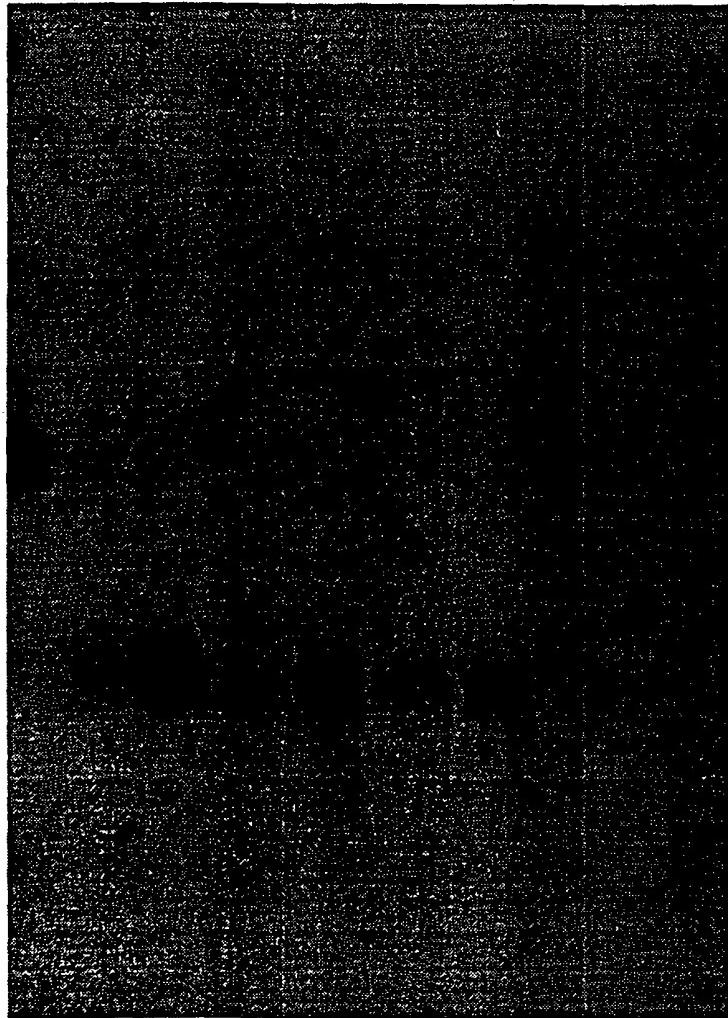


- 28S

- 18S

Fig. 1A



- 28S

- 18S

Fig. 1B

1 CTGGCTGCTGGAGTTGTGACATACTAGGTGACACCCCTGGAGTCACTTC
53 TCTTCAACTCCAGCTTAGAAGTGCTGCCTGGCTCAGGGTCTGCACTGCAGCCTACTCCT
113 TGCTTCAGGGCCTGACTGCAACGCCAAAGCCTATCCTATAGCGGCAGGCCAGGCCAC
173 TCAAACCAGCCACAGCTCCCCGCAACCGAACCATGAACACCGAAATGTATCAGACCCCC
MetAsnThrGluMetTyrGlnThrPro

233 ATGGAGGTGGCGGTCTATCAGCTGCACAATTCTCCACCTCCTTTCTCTGCTT
MetGluValAlaValTyrGlnLeuHisAsnPheSerThrSerPhePheSerSerLeuLeu

293 GGAGGGGATGTGGTTCCGTTAAACTGGATAACAGTGCCTCCGGAGCCAGTGTGGTGGCC
GlyGlyAspValValSerValLysLeuAspAsnSerAlaSerGlyAlaSerValValAla

353 CTAGACAACAAGATTGAGCAGGCCATGGACCTCGTGAAGAACCACCTGATGTACGCTGTG
LeuAspAsnLysIleGluGlnAlaMetAspLeuValLysAsnHisLeuMetTyrAlaVal

413 AGAGAGGAGGTGGAGGTCTAAAGGAGCAGATTGAGCTGCTTGAGAAGAACTCCCAG
ArgGluGluValGluValLeuLysGluGlnIleArgGluLeuLeuGluLysAsnSerGln

473 CTGGAGCGCGAGAACACCCCTCCTGAAGACGCTGGCAAGCCCCGAGCAACTGGAAAAGTTC
LeuGluArgGluLeuThrLeuLeuLysThrLeuAlaSerProGluGlnLeuGluLysPhe

533 CAGTCCCCGCTGAGCCCTGAAGAGCCAGCACCTGAAGCCCCAGAAACCCCCGAAACCCCG
GlnSerArgLeuSerProGluGluProAlaProGluAlaProGluThrProGluThrPro

593 GAAGCCCCCTGGTGGTCTGCGGTGTAAGTGGCTCTGTCCTTAGGGTGGGCAGGCCACAT
GluAlaProGlyGlySerAlaVal *

653 CTTGTTCTACCTAGTTCTTCCAGTTGGCTCCCAAGGGTCATCTCATGTGGA
713 GAACTTTACACCTAACATAGCTGGTCCAAGAGATGTCCTAACGGACATGCCCATCTGGGT
773 CCACTCCAGTGCAGAGACCCCTGACAAGAGCAGGTCTCTGGAGACTAAGTGCATGGGC
833 CTAGTAACACCAAGCCAGTGCAGGCTGTCGTGACCCCCCTGGGGCTCCAGGGCTG
893 GGCAACTTAGTTACAGCTGACCAAGGAGAAAGTAGTTTGAGATGTGATGCCAGTGTGCT
953 CCAGAAAAGTGAAGGGCTGTTTCAATTCCATGGACATCTTCCACAGCTTCACCTGA
1013 CAATGACTGTTCTATGAAGAACCCACTTGTGTTCTAACGAGAACCTCTCTCTTCT
1073 TCCTCTGTCTTCCAGGCAGGGCAGAGATGGGAGAGATTGAGCCAAATGAGCCTCTG
1113 TTGGTTAATACTGTATAATGCATGGCTTGTGACAGCCCAGTGTGGGTTACAGCTTG
1193 GGATGACTGCTTAAAGTTCTGTTGGTTAGTATTGGCATCGTTTCTATATAGCCAT
1253 AATGCGTATATATACCCATAGGCTAGATCTATATCTTAGGGTAGTGTATGATACATATA
1313 CACATACACCTACATGTTGAAGGGCTAACCGAGCTTGGGACTACTGACTGGTCTCTTAT
1373 CTCTTAAAGCTAAGTTTGACTGTGCTAATTACCAAATTGATCCAGTTGTCCCTTAG
1433 ATTAATAAGACTCGATATGAGGGAGGGAGGGAGACCAAGCAGCTCACAAATGCCAACAG
1493 ATGCCCTGCTGCTGCAGTCCTCCCTGATCTGCACTGAAGACATGAAGTCTCTTTG
1553 ATGCCAACCCACCATTCATTGGTGTGACTACATAGAATGGGTTGAGAGAACGATCAGT
1613 TTGGACTTCACATTGGTTAAAGTTAGGTTGTTTTGGTTTGTGTTTGT
1673 TTGTTGTTGTTGTTTGTGTTTTCTTTTAAAGTTCTGTGGGGAAACTTTGG
1733 GTTAATCAAAGGATGTAGTCCTGTGGTAGACCAGAGGAGTAACAGTTGATCCTTGG
1793 GGTGTGAAAATGTACCCAGGAAGCTGTGTAAGGAGGTTCTGTGACAGTGAACACTTC
1853 CACTTCTGACACCTCATCCTGCTGACACTCCAGGATTGGATTGGATTTCAAAT
1913 GTAGCTTGAATTCATAAACTTGCTCCTTTCTAAAAAATAAAAAAAAAAAAAA

Fig. 2

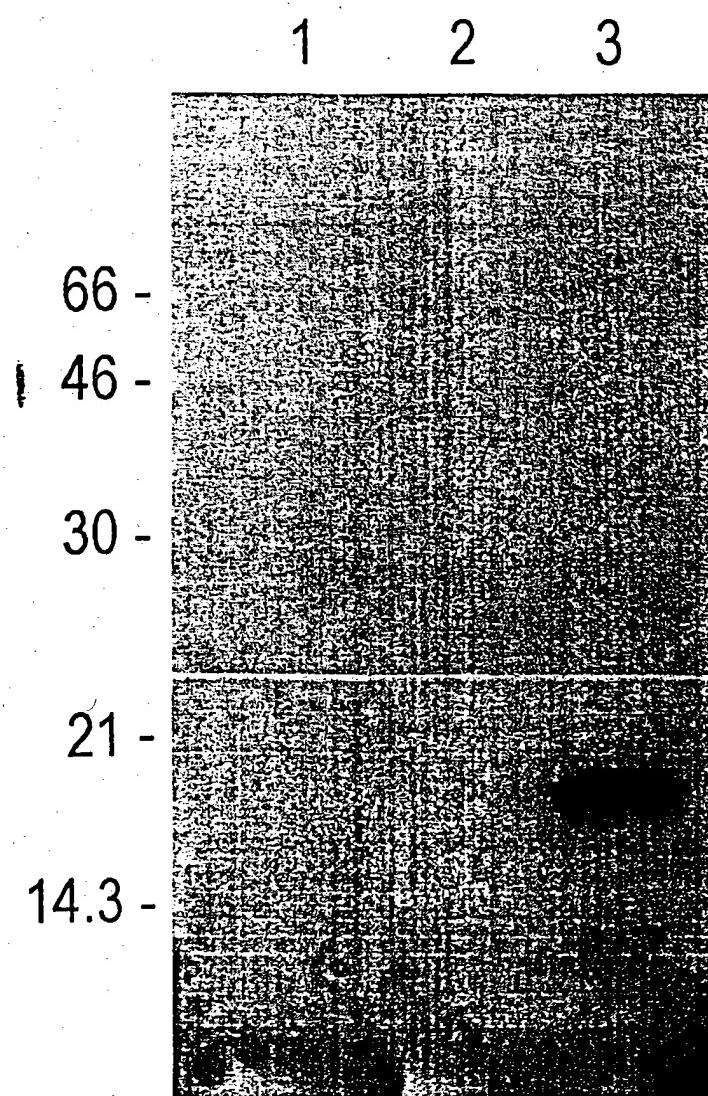


Fig. 3A

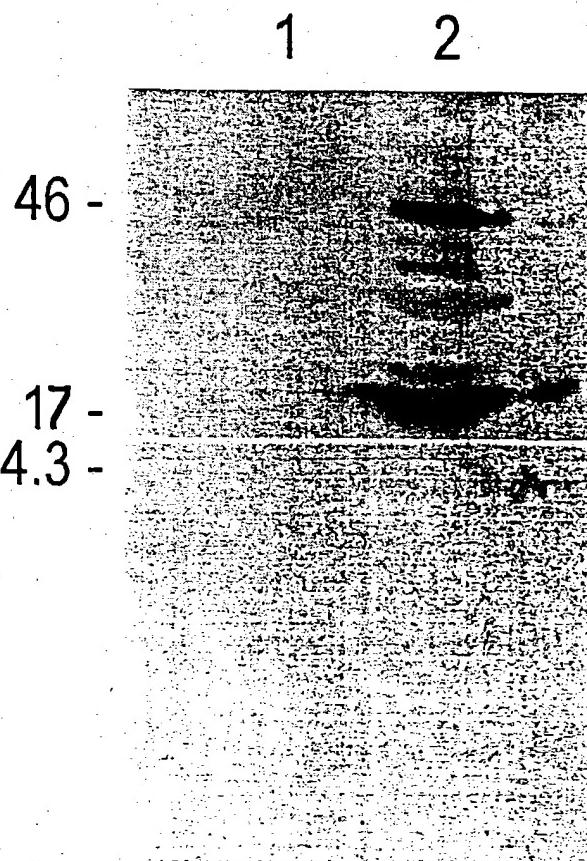


Fig. 3B

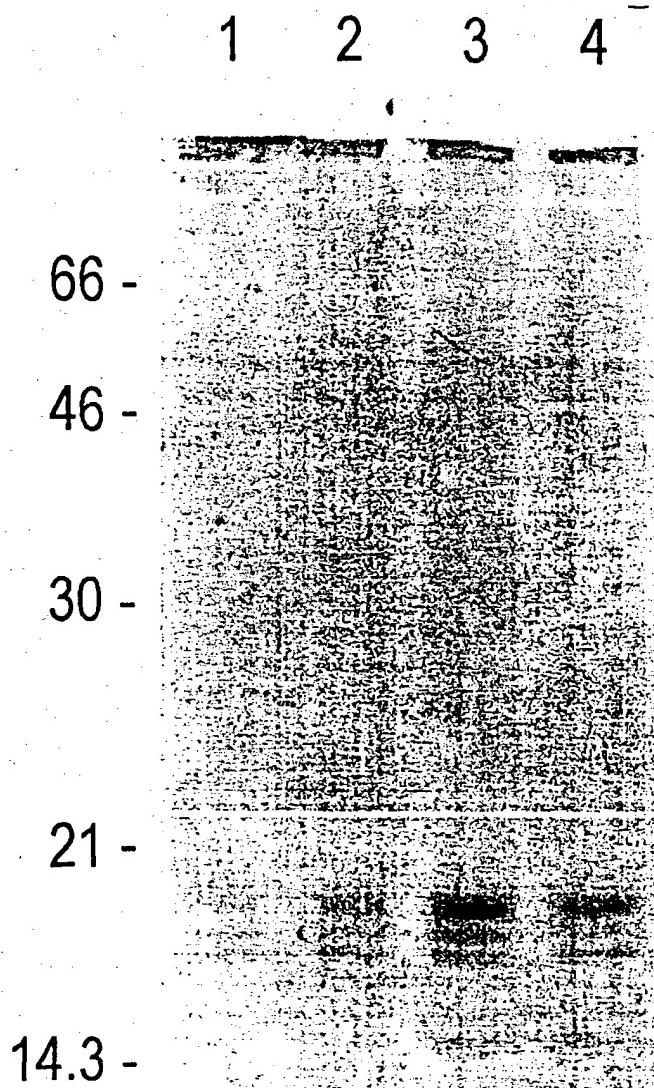


Fig. 3C

GILR	LKEQIRE	LLEKNSQ	LERENTL	LKT LA
TSC-22	LKEQIKE	LIEKNSQ	LEQENDL	LKT LA
GCN4	LEDKVVEE	LLSKNYH	LENEVARL	KKLV
CREB	LENRVAV	LENQNKT	LIEELKAL	KDLY
CREM	LENRVAV	LENQNKT	LIEELKAL	KDLY
c-jun	LEEKVKT	LKAQNSEL	LASTANML	REQV

Fig. 4

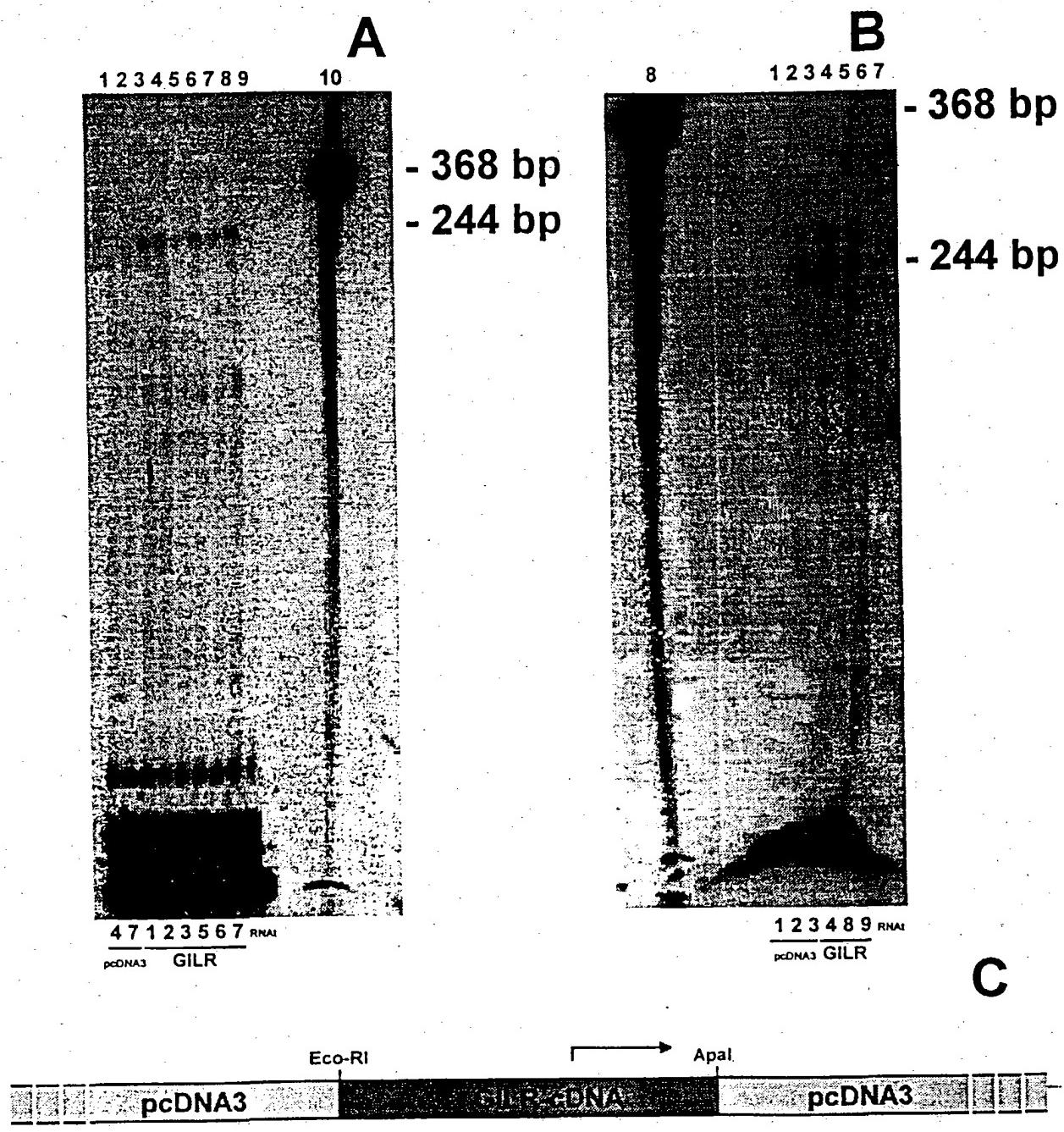


Fig. 5

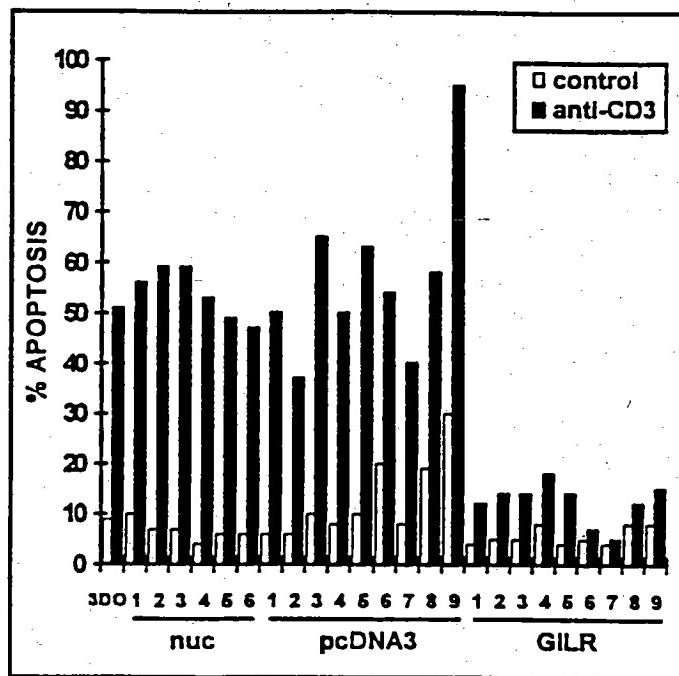


Fig. 6

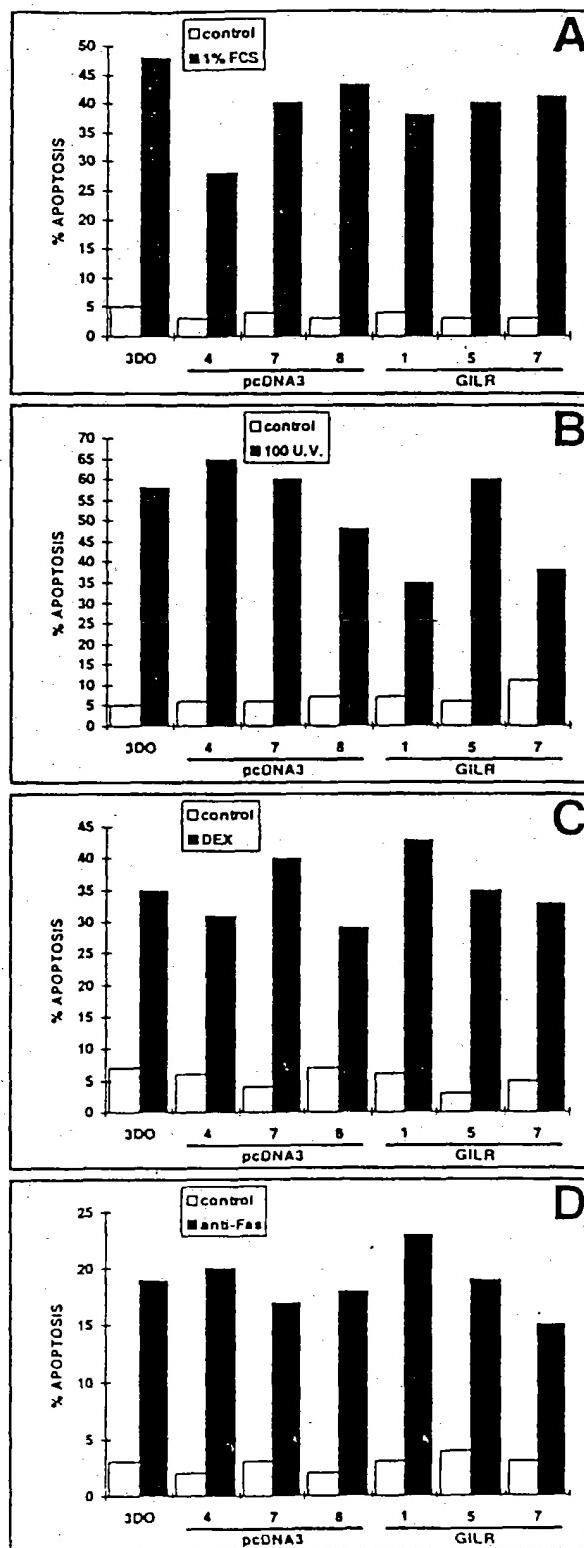


Fig. 7.

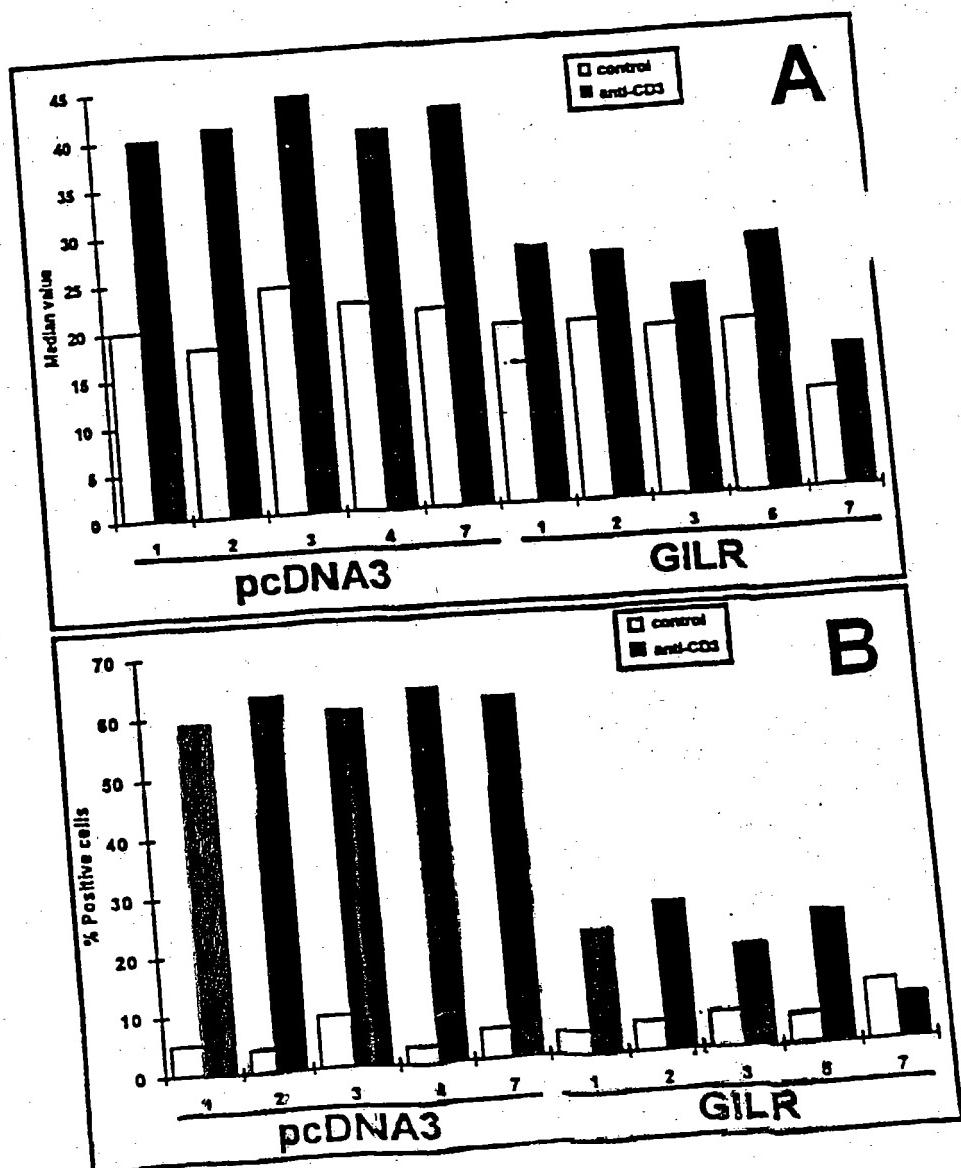


Fig.

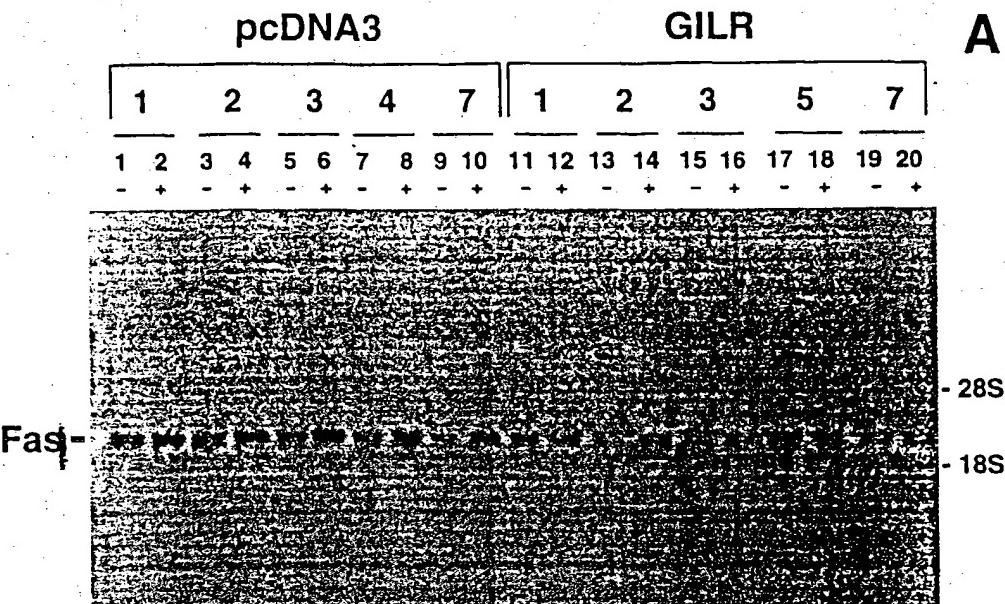
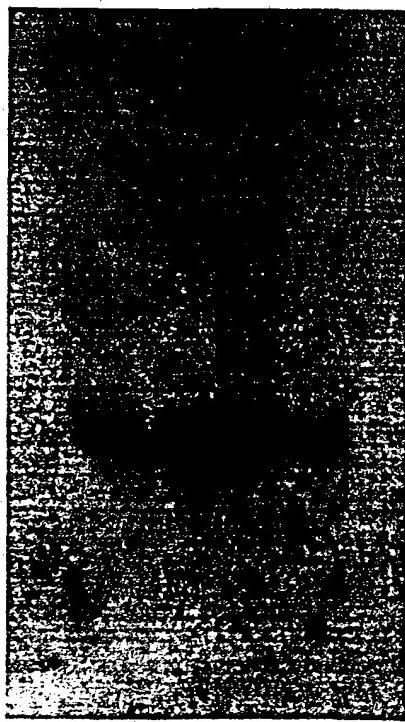
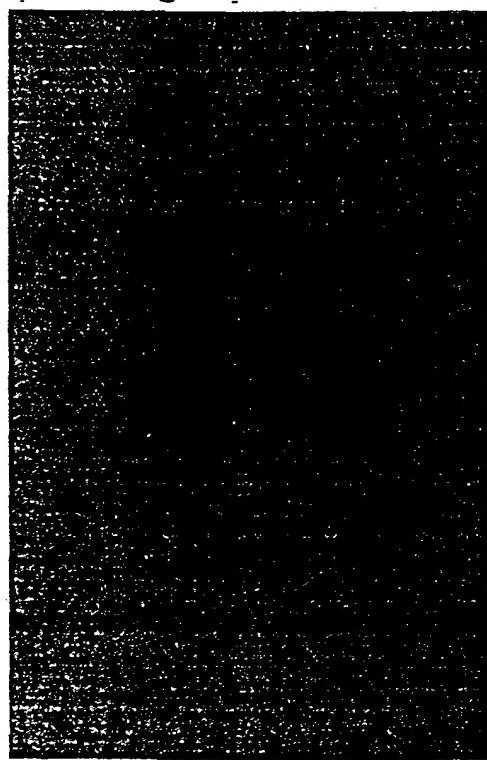


Fig. 9



A



B

Fig. 10

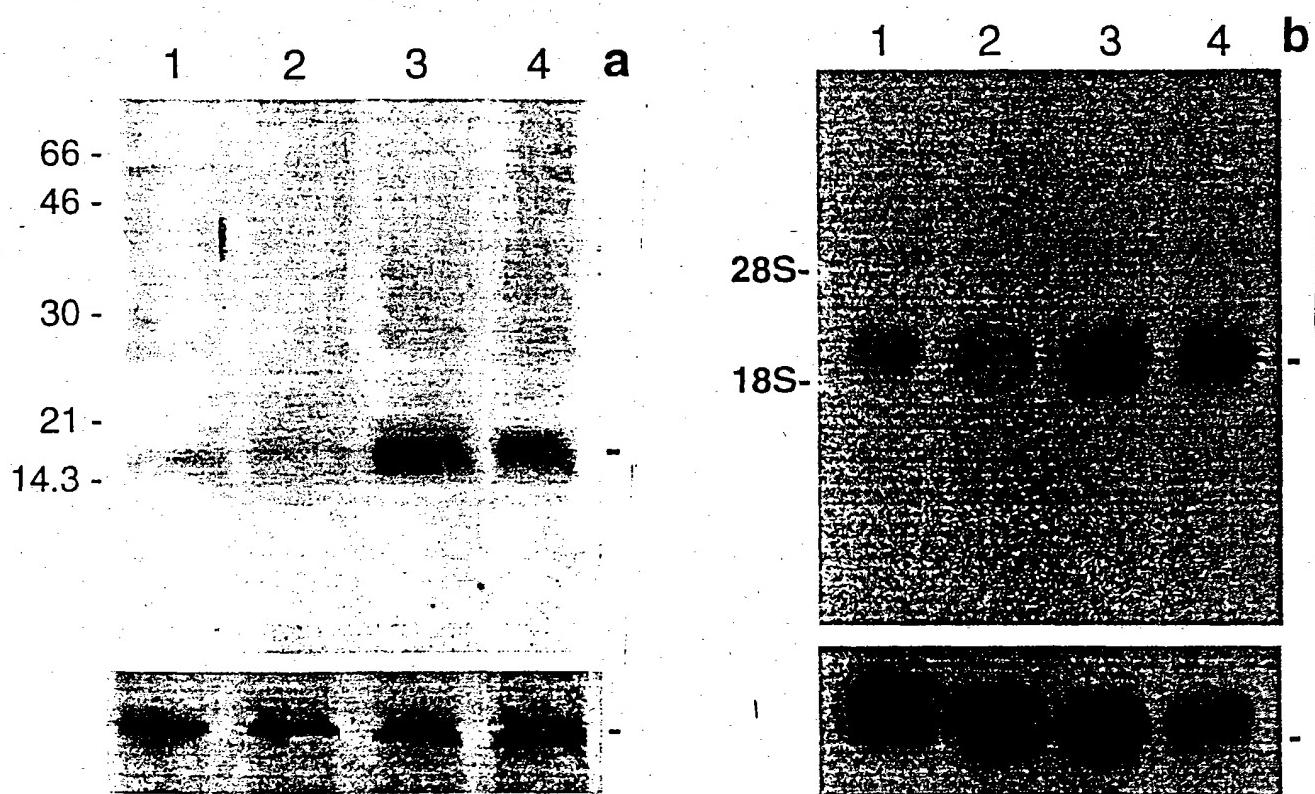


Fig. 11

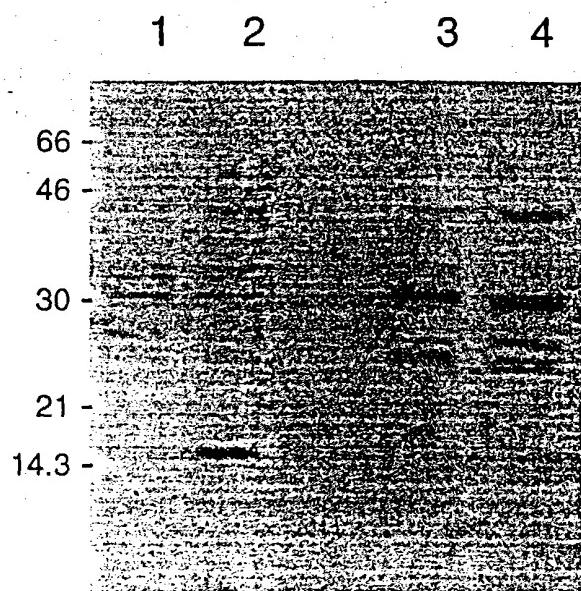
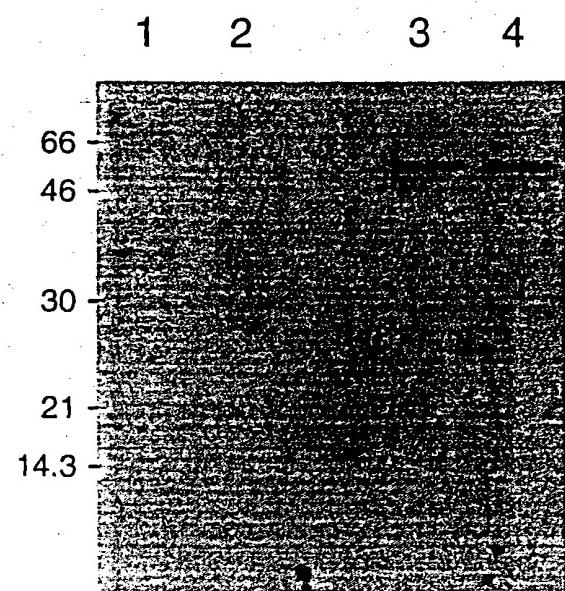
A**B**

Fig. 12

1 AATTGGGGGCCGTGGAGTTGTGACATACGAGGTGACACCCCTCGAGTCACTCCCTC
 61 AACTCCAGCTGGAGCGCCTGTTGGCTTGGGTTCTGCAGCCTTCGCCCCGCTCCT
 121 AGCCTCAGGGCCGGACTCCAGCGCAGAGCCCAGCCAGCGCAGCCTGCAGCAGCCACCC
 181 AGCCGCCAGCCGCCAGCCCCGACGAAACCCGCCAGAGCTCCTAGCAGCCCAGGCC
 241 ATGAACACCGAAATGTATCAGACCCCCATGGAGGTGGCGGTCTACCAGCTGCACAATTTC
 MetAsnThrGluMetTyrGlnThrProMetGluValAlaValTyrGlnLeuHisAsnPhe

 301 TCCATTCCTTCTTCTCTGCTGGAGGGATGTGGTTCCGTTAAGCTGGACAAC
 SerIleSerPhePheSerSerLeuLeuGlyGlyAspValValSerValLysLeuAspAsn

 361 AGTGCCTCCGGAGCCAGCGTGGTGGCCATAGACAACAAGATCGAACAGGCCATGGATCTG
 SerAlaSerGlyAlaSerValValAlaIleAspAsnLysIleAspGlnAlaMetAspLeu

 421 CTGAAGAACATCTGATGTATGCTGTGAGAGAGGGAGGTGGAGATCCTGAAGGAGCAGATC
 ValLysAsnHisLeuMetTyrAlaValArgGluGluValGluIleLeuLysGluGlnIle

 481 CGAGAGCTGGTGGAGAAGAACTCCCAGCTAGAGCGTGAGAACACCCCTGTTGAAGAGCCCTG
 ArgGluLeuValGluLysAsnSerGlnLeuGluArgGluAsnThrLeuLeuLysThrLeu

 541 GCAAGCCCAGAGCAGCTGGAGAAGTTCACTGCTGTCTGAGCCCTGAAGAGGCCAGCTCCC
 AlaSerProGluGlnLeuGluLysPheGlnSerCysLeuSerProGluGluProAlaPro

 601 GAATCCCCACAAGTCCCCAGGGCCCTGGTGGTCTGCGGTGTAAGTGGCTCTGCTCTCA
 GluSerProGlnValProGluAlaProGlyGlySerAlaVal *

 661 GGGTGGGCAGAGCCACTAAACTTGTACCTAGTTCTTCCAGTTGGTTGGCTCCC
 721 CAAGCATCATCTCACGAGGAGAACTTACACCTAGCACAGCTGGTGCAAGAGATGTCCT
 781 AAGGACATGGCCACCTGGGTCCACTCCAGCGACAGACCCCTGACAAGAGCAGGTCTCTGG
 841 AGGCTGAGTTGCATGGGCCTAGTAACACCAAGCCAGTGAGCCTCTAAATGCTACTGCGCC
 901 CTGGGGGCTCCAGGGCTGGCAACTTAGCTGCAACTGGCAAAGGAGAAGGGTAGTTG
 961 AGGTGTGACACCAGTTGCTCCAGAAAGTTAAGGGTCTGTTCTCATCTCCATGGACA
 1021 TCTTCAACAGCTTCACCTGACAACGACTGTTCTATGAAGAAGCCACTTGTGTTTAAGC
 1081 AGAGGCAACCTCTCTCTGTTCTGTTGTAAGGCAGGGACACAGATGGAGAGAT
 1141 TGAGCCAAGTCAGCCTCTGTTGTTAATATGGTATAATGCACTGGCTTGTGACAGCCC
 1201 AGTGTGGATTACAGCTTGGATGACCGCTTACAAAGTTCTGTTGGTTAGTATTGGCA
 1261 TAGTTTTCTATATAGCCATAATGCGTATATATACCCATAGGGCTAGATCTGTATCTTA
 1321 GTGTAGCGATGTATACATACACATCCACCTACATGTTGAAGGGCTAACCAGCCTGG
 1381 GAGTATTGACTGGTCCCTAACCTCTTATGGCTAAGTCTTGACTGTGTTCATTAACCAAG
 1441 TTGACCCAGTTGCTTTAGGTTAAGTAAGAACCTGAGAGTAAGGCAAGGAGGGGGC
 1501 CAGCCTCTGAATGCGGCCACGGATGCCCTGCTGCTGCAACCCCTTCCCCAGCTGTCAC
 1561 GAAACGTGAAGTCTGTTGAAATGCCAAACCCACCAATTCACTGGTGTGACTACATAGA
 1621 ATGGGTGAGAGAAGATCAGTTGGCTTACAGTGTCAATTGAAAAAGCGTTTGTGTT
 1681 TGTTTGAAATTATGAAAACCTTCAAGTGAACAGAAGGATGGTGTCTACTGTGGAT
 1741 GAGGGATGAACAAGGGGATGGCTTGTGATCCAATGGAGCCTGGGAGGTGTGCCCAGAAAGC
 1801 TTGTCTGTAGCGGGTTTGTGAGAGTGAACACTTCACTTTGACACCTTATCCTGAT
 1861 GTATGGTTCCAGGATTGGATTTGATTTCAAATGTAGCTTGAAATTCAATAACTT
 1921 TGCTCTGTTTCTAAAAAATAAAAA

Fig. 13

1 ...CTGGCTGCTGGAGTTGTGACATACTAGGTGACACCCCTGGAGTC 47
1 aattcgggggccgtggagttgtgacatacggaggtagacaccctcgagtc 50
48 ACTTCTCTCAACTCCAGCTTAGAAGTGCCTGCCTGGCTCAGGGCTGCA 97
51 acttccctcaactccagct..ggagcgcctgctggcttgggtcggt 98
98 CTGCAGCCT.....ACTCCTGCTTCAGGGCCTGACTGCAACGCCAAA 140
99 ctgcagccttcgccccgctctagcctcagggccggactccagcgcagag 148
141 GCCTATCC.....TATAGCGGCAGCGCCA 164
149 cccagcccagcgcagcctgcccagcagccacccagccgcccagcccccag 198
165 GCAGCCACTCAAACCAGCCACAGCTCCCCGGCA.ACCGAACCATAACAC 213
199 ccccgacgaaaccggccagagcttccctagcagcccgagccatgaacac 248
214 CGAAATGTATCAGACCCCCATGGAGGTGGCGGTCTATCAGCTGCACAATT 263
249 cgaardatgtatcagaccccatggagggtggcggtctaccagctgcacaatt 298
264 TCTCCACCTCCTCTTTCTCTCTGCTTGGAGGGGATGTGGTTCCGTT 313
299 tctccatctccttctctctgtggagggatgtgggtccgtt 348
314 AAACTGGATAAACAGTGCCTCCGGAGCCAGTGTGGTGGCCCTAGACAACAA 363
349 aagctggacaacagtgcctccggagccagcgtggcgatagacaacaa 398
364 GATTGAGCAGGCCATGGACCTCGTGAAGAACACCTGATGTACGCTGTGA 413
399 gatcgaacaggccatggatctggtaagaatcatctgtatgtatgtatgtga 448
414 GAGAGGAGGTGGAGGTCTAAAGGAGCAGATTGAGCTGAGCTGCTTGAGAAG 463
449 gagaggaggtggagatcctgatggtaagaatcatctgtatgtatgtatgtga 498
464 AACTCCCAGCTGGAGCGCGAGAACACCCCTCCTGAAGACGCTGGCAAGCCC 513
499 aactcccagctagagcgtgagaacacccctgttgaaagacccctggcaagccc 548
514 CGAGCAACTGGAAAAGTCCAGTCCCGGCTGAGCCCTGAAGAGGCCAGCAC 563
549 agagcagctggagaagttccagtcctgtctgagccctgaaagagccagctc 598
564 CTGAAGCCCCAGAAACCCGGAAACCCGGAAAGCCCTGGTGGTCTGCG 613
599 ccgaatccccca.....caagtggcccgaggccctgggtgggtctg 639

Fig. 14.

Fig. 14 (cont)

Fig. 14 (Cont.)

mG	1	MNTEMYQTPMEVAVYQLHNFSTSFSSLLGGDVSVKLDNSASGASVVAL	50
hG	1	MNTEMYQTPMEVAVYQLHNFSISFFSSLLGGDVSVKLDNSASGASVVAI	50
<hr/>			
hT	2	KSQWCRPVAMDLGVYQLRHFSISFLSSLLGTENASVRLDNSSSGASVVAI	51
<hr/>			
mG	51	DNKIEQAMDLVKNHLMYAVREEVEVLKEQIRELLEKNSQLERENTLLKTL	100
hG	51	DNKIEQAMDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL	100
<hr/>			
hT	52	DNKIEQAMDLVKSHLMYAVREEVEVLKEQIKELIEKNSQLEQENNLLKTL	101
<hr/>			
hD	1	MDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL	41
<hr/>			
mG	101	ASPEQLEKFQSRLSPEEPAPEAPETPETPEAPGGSAV*	138
hG	101	ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGSAV*	135
<hr/>			
hT	102	ASPEQLAQFQAQLQTGSPPATTQPQGTTQPPAQPAQSGSGPTA*	145
<hr/>			
hD	42	ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGSAV*	
<hr/>			

Fig. 15

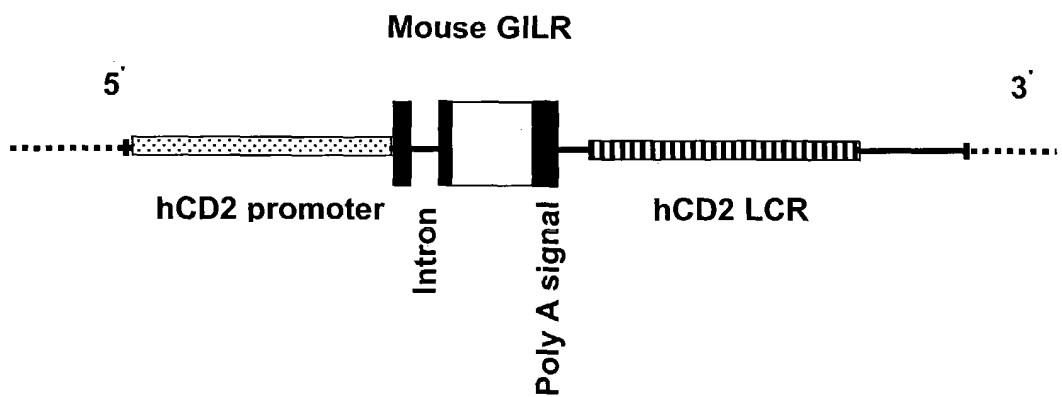


FIG. 16A

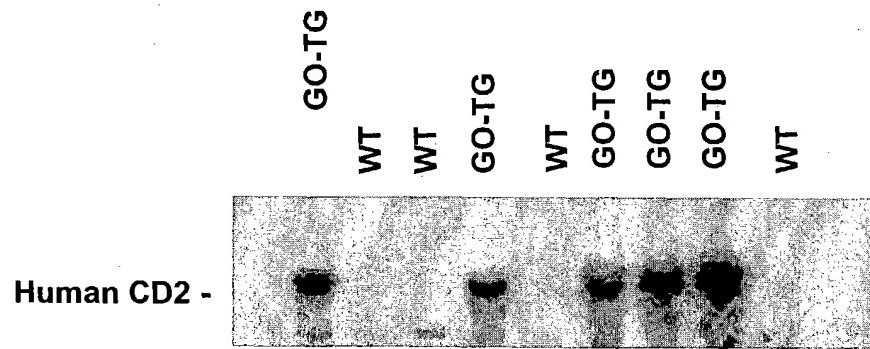


FIG. 16B

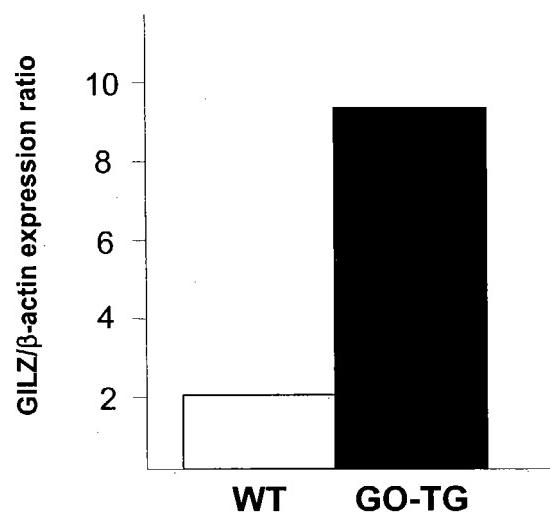


FIG. 17A

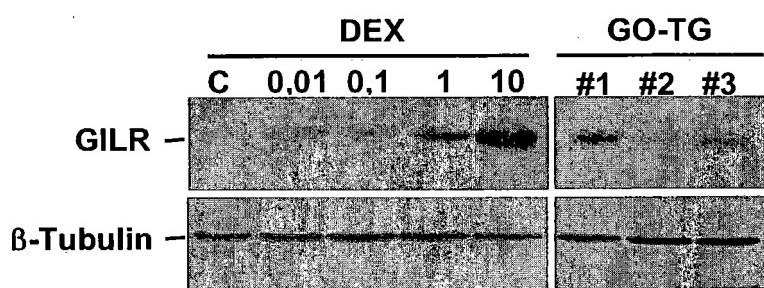
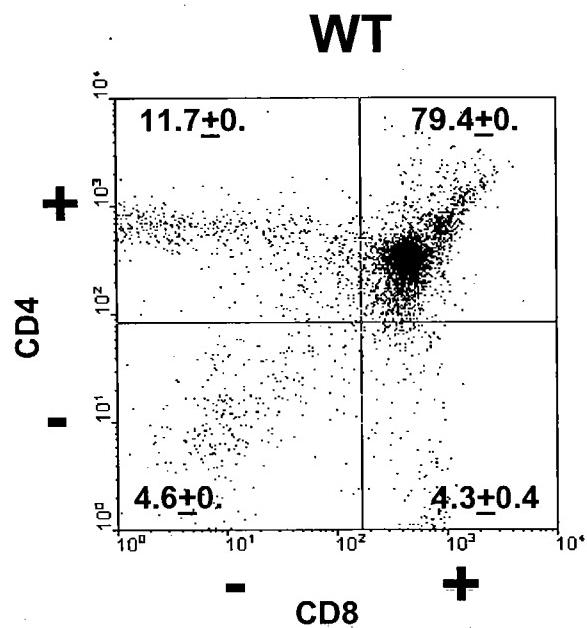


FIG. 17B

FIG. 18A



GO-TG

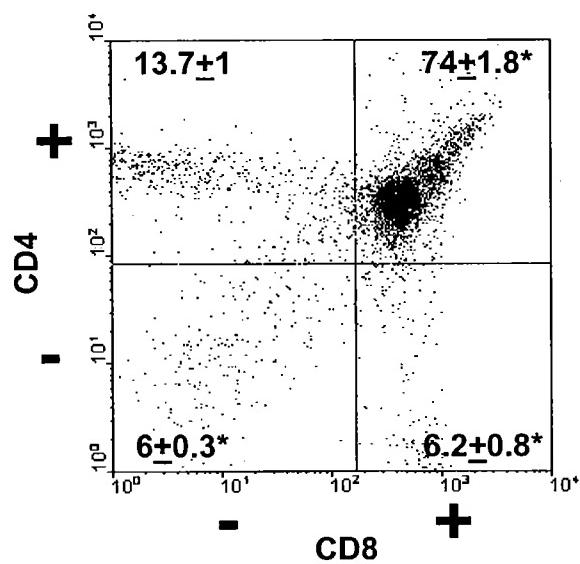
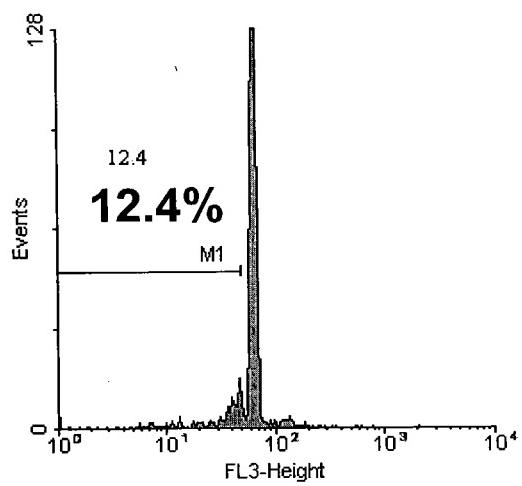


FIG. 18B

WT



GO-TG

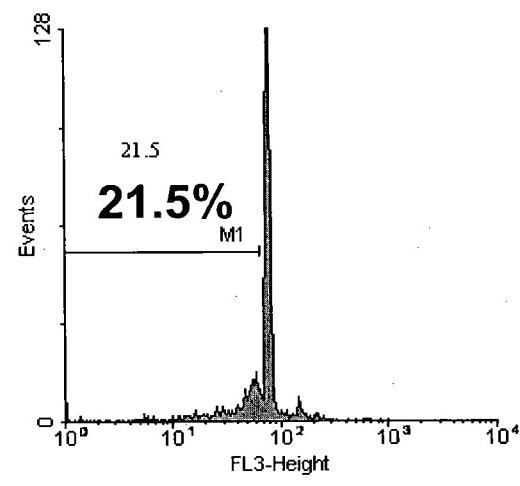


FIG. 19A

FIG. 19B

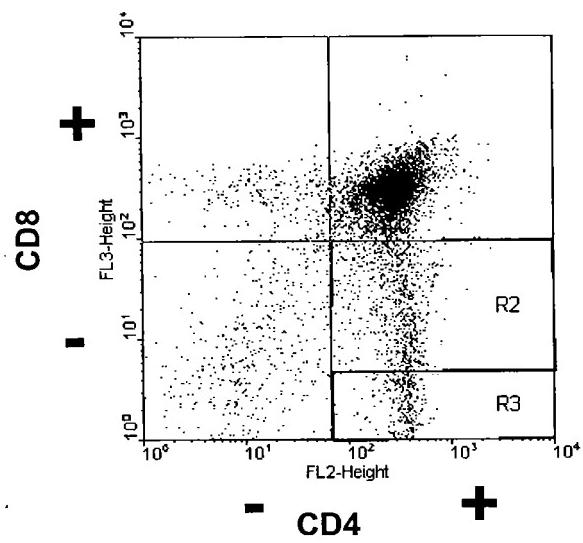


FIG. 20A

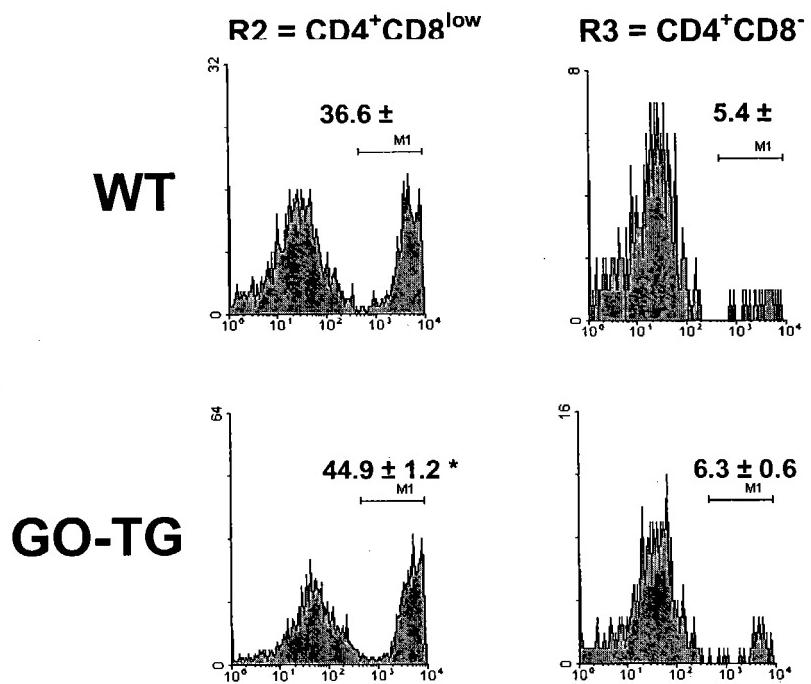


FIG. 20B

FIG. 21A

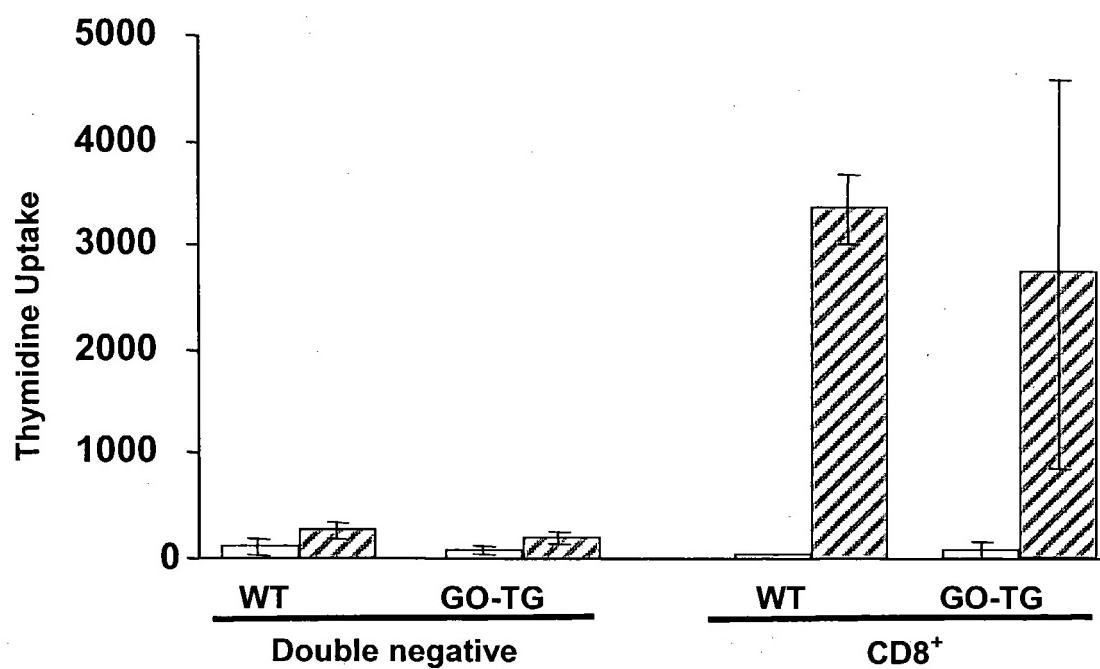
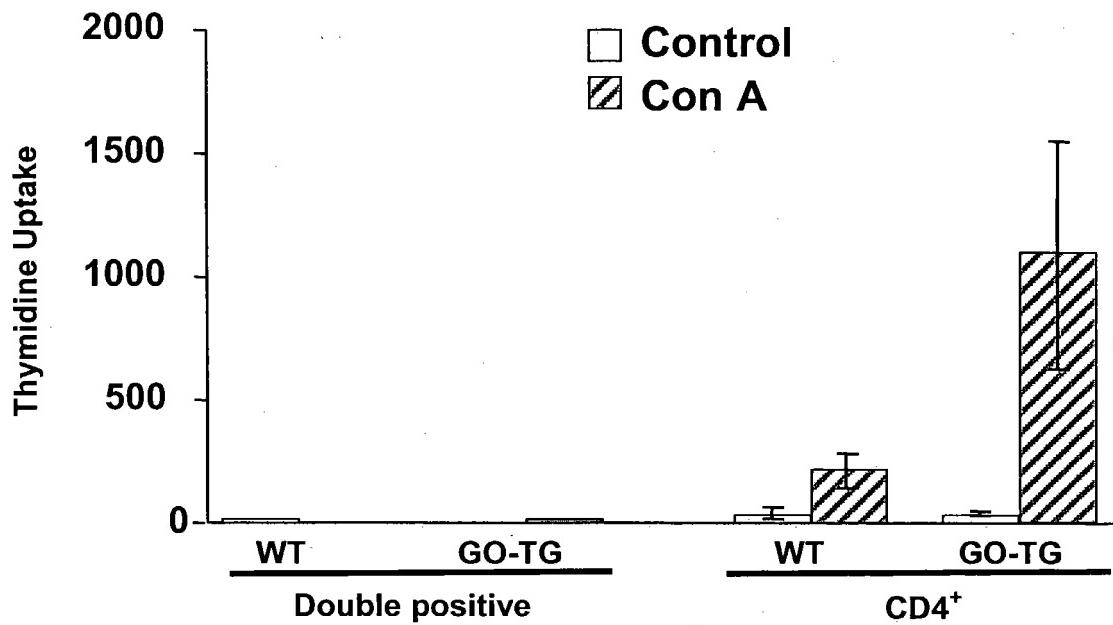


FIG. 21B

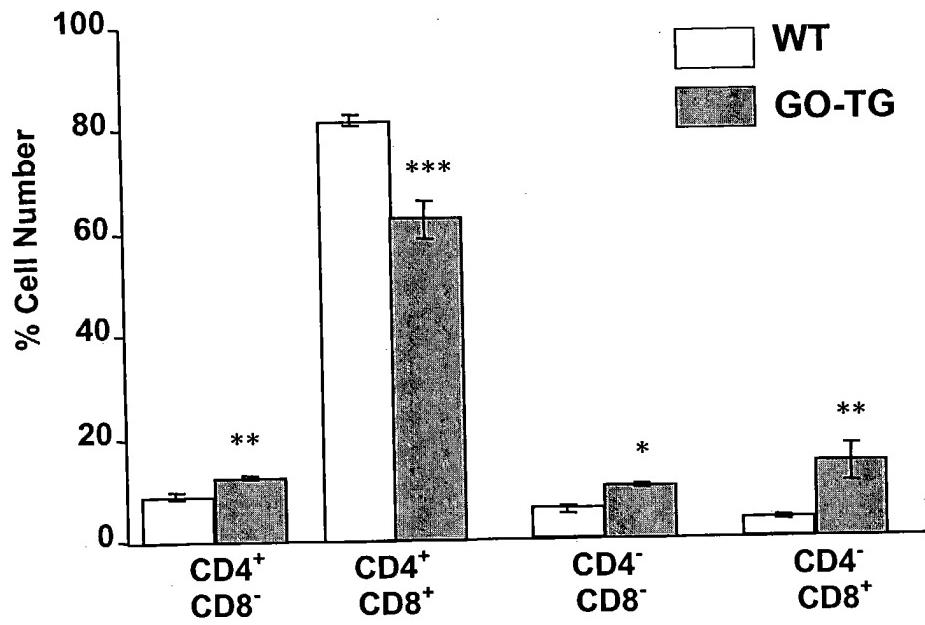


FIG. 22

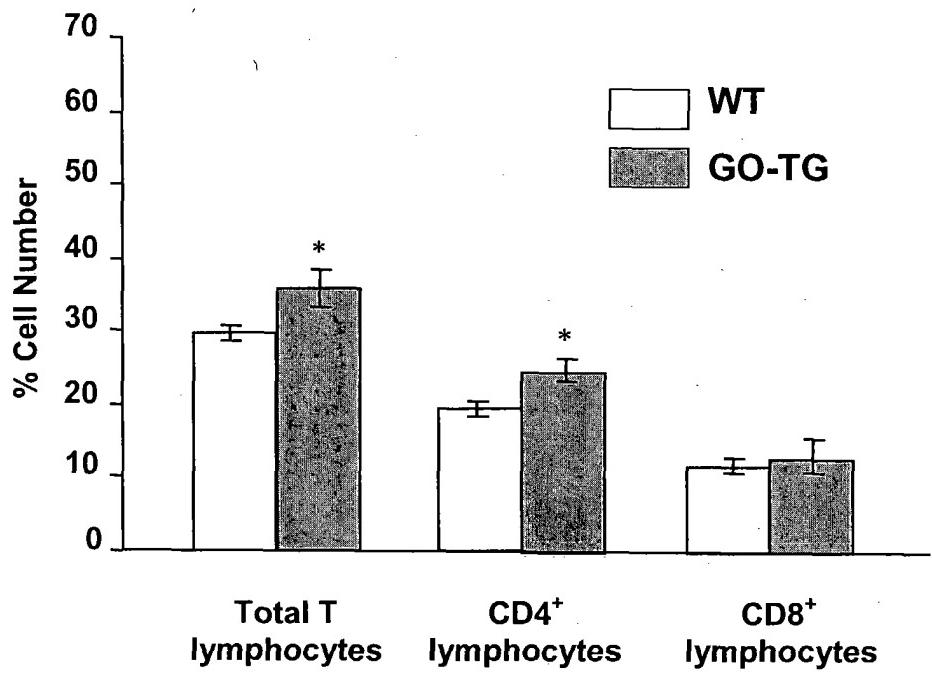


FIG. 23

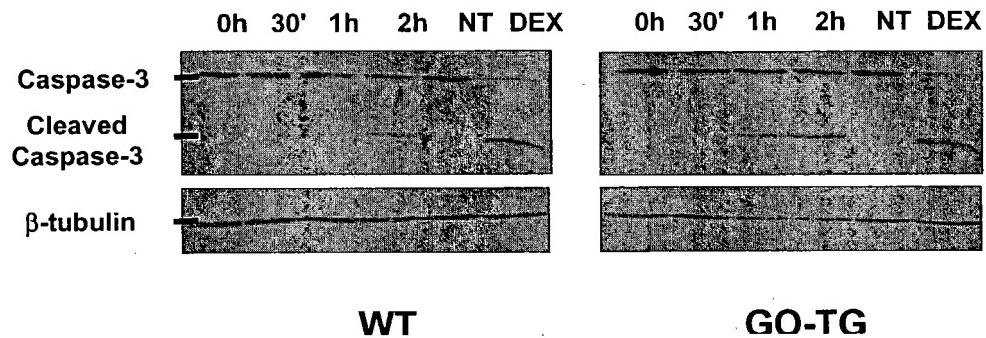


FIG. 24